

80

SEQUENCE LISTING

<110> Acton, Susan

<120> NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

<130> MNI-050

<140>

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<160> 15

<170> PatentIn Ver. 2.0

<210> 1

<211> 4137

<212> DNA

<213> Homo sapiens

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<223> 'n' at positions 2872, 3597 and 3682 may be any nucleic acid

<220>

<221> CDS

<222> (297)..(1202)

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gcggcgccggc gggaggtggc cgacaggctc cgggcctcgc agcctcagcc cccggcccag 180
cgcgctttcc gacggcggcg ccgcgccgag ccacccgccc gcccaaggtc tctcggggc 240
gggagaacgg aaaactccca acttctgag ttctaaagtt cctgttgctt cagaca atg 299
                                         Met
                                         1

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gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc caa 347
Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe Gln
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cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc aac 395
Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala Asn
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ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt tat 443
Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr
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aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa gtg 491
Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys Val
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cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc aaa 539

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81

Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile Lys	
70 75 80	
gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa tat	587
Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys Tyr	
85 90 95	
tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa cta	635
Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu	
100 105 110	
gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag caa	683
Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys Gln	
115 120 125	
aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag ctt	731
Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu	
130 135 140 145	
tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga gat	779
Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg Asp	
150 155 160	
ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa ctt	827
Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu	
165 170 175	
gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct gca	875
Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala Ala	
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cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata cat	923
His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His	
195 200 205	
gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt cta	971
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu	
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cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa atg	1019
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met	
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Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro	
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Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Met	
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Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val Tyr	
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Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser	

82

290 295 300

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acaattgtga acttttgtga agattttatt tttaaacggt tgaagtacta gtttttagttc 1692

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83

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84

35 40 45
 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
 50 55 60
 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
 65 70 75 80
 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
 85 90 95
 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
 100 105 110
 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
 115 120 125
 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
 130 135 140
 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
 145 150 155 160
 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
 165 170 175
 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
 180 185 190
 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
 195 200 205
 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
 210 215 220
 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
 225 230 235 240
 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
 245 250 255
 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
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<222> (1)..(906)

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caa cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc 96
Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
             20             25             30

aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt 144
Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
             35             40             45

tat aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa 192
Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
             50             55             60

gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc 240
Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
             65             70             75             80

aaa gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa 288
Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
             85             90             95

tat tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa 336
Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
             100            105            110

cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag 384
Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
             115            120            125

caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag 432
Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
             130            135            140

ctt tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga 480
Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
             145            150            155            160

gat ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa 528
Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
             165            170            175

ctt gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct 576
Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
             180            185            190

gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata 624
Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
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cat gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt 672

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86

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His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
 210                               215                               220

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Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
225                               230                               235                               240

atg aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca   768
Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
                245                               250                               255

cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat   816
Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
                260                               265                               270

atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt   864
Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val
                275                               280                               285

tat gac gta gca aag agg atg cat gca tgc act gca agc agc           906
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<220>
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 <222> (47)..(1411)

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Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu Gln Phe Phe
   5                               10                               15

gaa aac tgc ggt gga gga agt ttt ggg agt gtt tat cga gcc aaa tgg   151
Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg Ala Lys Trp
 20                               25                               30                               35

ata tca cag gac aag gag gtg gct gta aag aag ctc ctc aaa ata gag   199
Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu Lys Ile Glu
                40                               45                               50

aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac atc atc cag   247
Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn Ile Ile Gln
                55                               60                               65

ttt tat gga gta att ctt gaa cct ccc aac tat ggc att gtc aca gaa   295
Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile Val Thr Glu
 70                               75                               80

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87

tat gct tct ctg gga tca ctc tat gat tac att aac agt aac aga agt	343
Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser Asn Arg Ser	
85 90 95	
gag gag atg gat atg gat cac att atg acc tgg gcc act gat gta gcc	391
Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr Asp Val Ala	
100 105 110 115	
aaa gga atg cat tat tta cat atg gag gct cct gtc aag gtg att cac	439
Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys Val Ile His	
120 125 130	
aga gac ctc aag tca aga aac gtt gtt ata gct gct gat gga gta ctg	487
Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp Gly Val Leu	
135 140 145	
aag atc tgt gac ttt ggt gcc tct cgg ttc cat aac cat aca aca cac	535
Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His Thr Thr His	
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atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa gtt atc cag	583
Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu Val Ile Gln	
165 170 175	
agt ctc cct gtg tca gaa act tgt gac aca tat tcc tat ggt gtg gtt	631
Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr Gly Val Val	
180 185 190 195	
ctc tgg gag atg cta aca agg gag gtc ccc ttt aaa ggt ttg gaa gga	679
Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly Leu Glu Gly	
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tta caa gta gct tgg ctt gta gtg gaa aaa aac gag aga tta acc att	727
Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg Leu Thr Ile	
215 220 225	
cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat cag tgt tgg	775
Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His Gln Cys Trp	
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gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc att tca atc	823
Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile Ile Ser Ile	
245 250 255	
ctg gag tcc atg tca aat gac acg agc ctt cct gac aag tgt aac tca	871
Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys Cys Asn Ser	
260 265 270 275	
ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag gca act ctt	919
Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu Ala Thr Leu	
280 285 290	
gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag gag cag gag	967
Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys Glu Gln Glu	
295 300 305	

88

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 310 315 320

gag cag tcc aac acc ccg ctt ctc ttg cct ctt gct gca aga atg tct 1063
 Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala Arg Met Ser
 325 330 335

gag gag tct tac ttt gaa tct aaa aca gag gag tca aac agt gca gag 1111
 Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn Ser Ala Glu
 340 345 350 355

atg tca tgt cag atc aca gca aca agt aac ggg gag ggc cat ggc atg 1159
 Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly His Gly Met
 360 365 370

aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg gat atc ttc 1207
 Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly Asp Ile Phe
 375 380 385

tca atg aac aaa gca gga gct gtg atg cat tct ggg atg cag ata aac 1255
 Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met Gln Ile Asn
 390 395 400

atg caa gcc aag cag aat tct tcc aaa acc aca tct aag aga agg ggg 1303
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 405 410 415

aag aaa gtc aac atg gct ctg ggg ttc agt gat ttt gac ttg tca gaa 1351
 Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp Leu Ser Glu
 420 425 430 435

ggt gac gat gat gat gat gat gac ggt gag gag gag gat aat gac atg 1399
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 440 445 450

gat aat agt gaa tgaaagcaga aagcaaagta ataaaatcac aaatgtttgg 1451
 Asp Asn Ser Glu
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89

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<400> 5

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 35 40 45
 Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn
 50 55 60
 Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile
 65 70 75 80
 Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser
 85 90 95
 Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr
 100 105 110
 Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys
 115 120 125
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 130 135 140
 Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His
 145 150 155 160
 Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu
 165 170 175
 Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr
 180 185 190
 Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly
 195 200 205
 Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg
 210 215 220
 Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His

90

225 230 235 240
 Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile
 245 250 255
 Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys
 260 265 270
 Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu
 275 280 285
 Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys
 290 295 300
 Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln
 305 310 315 320
 Lys Leu Thr Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala
 325 330 335
 Arg Met Ser Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn
 340 345 350
 Ser Ala Glu Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly
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 His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly
 370 375 380
 Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met
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 Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys
 405 410 415
 Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp
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Gln Phe Phe Glu Asn Cys Gly Gly Gly Ser Phe Gly Ser Val Tyr Arg				
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gcc aaa tgg ata tca cag gac aag gag gtg gct gta aag aag ctc ctc				144
Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu				
	35	40	45	
aaa ata gag aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac				192
Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn				
	50	55	60	
atc atc cag ttt tat gga gta att ctt gaa cct ccc aac tat ggc att				240
Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile				
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gtc aca gaa tat gct tct ctg gga tca ctc tat gat tac att aac agt				288
Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser				
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aac aga agt gag gag atg gat atg gat cac att atg acc tgg gcc act				336
Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr				
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gat gta gcc aaa gga atg cat tat tta cat atg gag gct cct gtc aag				384
Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys				
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Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp				
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Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His				
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aca aca cac atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa				528
Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu				
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Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr				
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Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly				
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Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg				
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Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His				
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92

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cat ggc atg aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly 370 375 380	1152
gat atc ttc tca atg aac aaa gca gga gct gtg atg cat tct ggg atg Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met 385 390 395 400	1200
cag ata aac atg caa gcc aag cag aat tct tcc aaa acc aca tct aag Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys 405 410 415	1248
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93

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Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
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ggc ccg gcg gcg ggc tgt gtc cgc ggg gag cgt cca ggc tgg gcc gca      200
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Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
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ctc cgc ttc ttc cgc cag tcg gtg gcc ggg ctg gcg gcg cgg ttg cag      296
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Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
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Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys
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Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
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cgc ttg cag ggc ttt cgg ctg gag gag tat ctg ata ggg cag tcc att      536
Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
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Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu

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94

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cca gcg agc cga gtg gcc Pro Ala Ser Arg Val 245	ttg gct ggg gag tat Leu Ala Gly Glu Tyr 250	gga gca gtc act tac Gly Ala Val Thr Tyr 255	824
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gcc ctg gtc gac tac cct Ala Leu Val Asp Tyr 295	gat gtg ctg ccc tca Pro Asp Val Leu Pro 300	cgc ctc cac cct gaa Arg Leu His Pro Glu 305	968
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96

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Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro
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Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys
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Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu
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Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile
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Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp
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Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln
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Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro
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Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro
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97

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 Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu
 225 230 235 240
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 260 265 270
 Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu
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 Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His
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 Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn
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 Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro
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 Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe
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 Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro
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 Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly
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 Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg
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 Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro
 465 470 475 480
 Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys
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98

Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp
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Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val
 515 520 525

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 Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys
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99

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Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His	
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100

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Asp	Val	Arg	Gln	Leu	Val	Arg	Ala	Leu	Leu	Gln	Arg	Glu	Ala	Ser	Lys		
			485					490						495			
aga	cca	tct	gcc	cga	gta	gcc	gca	aat	gtg	ctt	cat	cta	agc	ctc	tgg	1536	
Arg	Pro	Ser	Ala	Arg	Val	Ala	Ala	Asn	Val	Leu	His	Leu	Ser	Leu	Trp		
			500					505					510				
ggt	gaa	cat	att	cta	gcc	ctg	aag	aat	ctg	aag	tta	gac	aag	atg	gtt	1584	
Gly	Glu	His	Ile	Leu	Ala	Leu	Lys	Asn	Leu	Lys	Leu	Asp	Lys	Met	Val		
		515				520						525					
ggc	tgg	ctc	ctc	caa	caa	tcg	gcc	gcc	act	ttg	ttg	gcc	aac	agg	ctc	1632	
Gly	Trp	Leu	Leu	Gln	Gln	Ser	Ala	Ala	Thr	Leu	Leu	Ala	Asn	Arg	Leu		
	530					535						540					
aca	gag	aag	tgt	tgt	gtg	gaa	aca	aaa	atg	aag	atg	ctc	ttt	ctg	gct	1680	
Thr	Glu	Lys	Cys	Cys	Val	Glu	Thr	Lys	Met	Lys	Met	Leu	Phe	Leu	Ala		
545					550					555					560		
aac	ctg	gag	tgt	gaa	acg	ctc	tgc	cag	gca	gcc	ctc	ctc	ctc	tgc	tca	1728	
Asn	Leu	Glu	Cys	Glu	Thr	Leu	Cys	Gln	Ala	Ala	Leu	Leu	Leu	Cys	Ser		

101

565 570 575 1743

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Trp Arg Ala Ala Leu
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gaacatgtat tgaattggac ttagctgaac aggctgctgg ttggctgccc agaggggggca 180
ggctgtgttg ctgggagcct tccagctccc tgcagcagtc atggggcagg gttccccgag 240
tccgtaatcc ccatttccac ctactttccc ttag tta ttt gat tcc ctg tct gtc 295
Leu Phe Asp Ser Leu Ser Val
1 5

gta ctc agc tta agt gga gca tcc cct ttc ctg gga gac acg aag cag 343
Val Leu Ser Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln
10 15 20

gaa aca ctg gca aat atc aca gca gtg agt tac gac ttt gat gag gaa 391
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu
25 30 35

ttc ttc agc cag acg agc gag ctg gcc aag gac ttt att cgg aag ctt 439
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu
40 45 50 55

ctg gtt aaa gag acc cgg aaa cgg ctc aca atc caa gag gct ctc aga 487
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg
60 65 70

cac ccc tgg atc acg ccg gtg gac aac cag caa gcc atg gtg cgc agg 535
His Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg
75 80 85

gag tct gtg gtc aat ctg gag aac ttc agg aag cag tat gtc cgc agg 583
Glu Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg
90 95 100

cgg tgg aag ctt tcc ttc agc atc gtg tcc ctg tgc aac cac ctc acc 631
Arg Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr
105 110 115

102

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cgc tcg ctg atg aag aag gtg cac ctg agg ccg gat gag gac ctg agg 679
Arg Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg
120                      125                      130                      135

aac tgt gag agt gac act gag gag gac atc gcc agg agg aaa gcc ctc 727
Asn Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu
                      140                      145                      150

cac cca cgg agg agg agc agc acc tcc taactggcct gacctgcagt. 774
His Pro Arg Arg Arg Ser Ser Thr Ser
                      155                      160

ggccgccagg gaggtctggg ccagcggggg ctcccttctg tgcagacttt tggacccagc 834
tcagcaccag caccggggcg tcctgagcac ttgcaagag agatgggccc aaggaattca 894
gaagagcttg caggcaagcc aggagaccct gggagctgtg gctgtcttct gtggaggagg 954
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caaaaaatc aaaaaattag ccaggtgtag gggtaggcac ctggcatccc agctactcca 1734
ggggctgagg tgacagcatt gcttaagccc agaaggtcga ggctgcagtg agctgagatc 1794
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gggcggccgc 1864

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<212> PRT
<213> Homo sapiens

<400> 11

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103

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 Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala
 35 40 45
 Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu
 50 55 60
 Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn
 65 70 75 80
 Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe
 85 90 95
 Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu Ser Phe Ser Ile Val
 100 105 110
 Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu
 115 120 125
 Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp
 130 135 140
 Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Arg Ser Ser Thr Ser
 145 150 155 160

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 ttc ctg gga gac acg aag cag gaa aca ctg gca aat atc aca gca gta 96
 Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val
 20 25 30
 agt tac gac ttt gat gag gaa ttc ttc agc cag acg agc gag ctg gcc 144
 Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala
 35 40 45
 aag gac ttt att cgg aag ctt ctg gtt aaa gag acc cgg aaa cgg ctc 192
 Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu
 50 55 60

104

aca atc caa gag gct ctc aga cac ccc tgg atc acg ccg gtg gac aac 240
 Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn
 65 70 75 80

cag caa gcc atg gtg cgc agg gag tct gtg gtc aat ctg gag aac ttc 288
 Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe
 85 90 95

agg aag cag tat gtc cgc agg cgg tgg aag ctt tcc ttc agc atc gtg 336
 Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu Ser Phe Ser Ile Val
 100 105 110

tcc ctg tgc aac cac ctc acc cgc tgc ctg atg aag aag gtg cac ctg 384
 Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu
 115 120 125

agg ccg gat gag gac ctg agg aac tgt gag agt gac act gag gag gac 432
 Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp
 130 135 140

atc gcc agg agg aaa gcc ctc cac cca cgg agg agg agc agc acc tcc 480
 Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Arg Ser Ser Thr Ser
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<210> 13

<211> 1333

<212> DNA

<213> Homo sapiens

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<222> (2)..(1333)

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 Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn
 1 5 10 15

cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca 97
 Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser
 20 25 30

gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat 145
 Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp
 35 40 45

ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct 193
 Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala
 50 55 60

cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg 241
 Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly
 65 70 75 80

ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa 289
 Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu

105

85										90					95					
gga	acc	ttg	atg	att	aga	gag	acg	tct	gga	gag	aag	aag	cga	tct	ggc	337				
Gly	Thr	Leu	Met	Ile	Arg	Glu	Thr	Ser	Gly	Glu	Lys	Lys	Arg	Ser	Gly					
100					105					110										
cac	agt	gac	agc	aat	ggc	ttt	gct	ggc	cac	atc	aac	ctc	cct	gac	ctg	385				
His	Ser	Asp	Ser	Asn	Gly	Phe	Ala	Gly	His	Ile	Asn	Leu	Pro	Asp	Leu					
115					120					125										
gtg	cag	cag	agc	cat	tct	cca	gct	gga	acc	ccg	act	gag	gga	ctg	ggg	433				
Val	Gln	Gln	Ser	His	Ser	Pro	Ala	Gly	Thr	Pro	Thr	Glu	Gly	Leu	Gly					
130					135					140										
cgc	gtc	tca	acc	cat	tcc	cag	gag	atg	gac	tct	ggg	act	gaa	tat	ggc	481				
Arg	Val	Ser	Thr	His	Ser	Gln	Glu	Met	Asp	Ser	Gly	Thr	Glu	Tyr	Gly					
145	150					155					160									
atg	ggg	agc	agc	acc	aaa	gcc	tcc	ttc	acc	ccc	ttt	gtg	gac	ccc	aga	529				
Met	Gly	Ser	Ser	Thr	Lys	Ala	Ser	Phe	Thr	Pro	Phe	Val	Asp	Pro	Arg					
165					170					175										
gta	tac	cag	acg	tct	ccc	act	gat	gaa	gat	gaa	gag	gat	gag	gaa	tca	577				
Val	Tyr	Gln	Thr	Ser	Pro	Thr	Asp	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Ser					
180					185					190										
tca	gcc	gca	gct	ctg	ttt	act	agc	gaa	ctt	ctt	agg	caa	gaa	cag	gcc	625				
Ser	Ala	Ala	Ala	Leu	Phe	Thr	Ser	Glu	Leu	Leu	Arg	Gln	Glu	Gln	Ala					
195					200					205										
aaa	ctc	aat	gaa	gca	aga	aag	att	tcg	gtg	gta	aat	gta	aac	cca	acc	673				
Lys	Leu	Asn	Glu	Ala	Arg	Lys	Ile	Ser	Val	Val	Asn	Val	Asn	Pro	Thr					
210					215					220										
aac	att	cgg	cct	cat	agc	gac	aca	cca	gaa	atc	aga	aaa	tac	aag	aaa	721				
Asn	Ile	Arg	Pro	His	Ser	Asp	Thr	Pro	Glu	Ile	Arg	Lys	Tyr	Lys	Lys					
225	230					235					240									
cga	ttc	aac	tca	gaa	ata	ctt	tgt	gca	gct	ctg	tgg	ggt	gta	aac	ctt	769				
Arg	Phe	Asn	Ser	Glu	Ile	Leu	Cys	Ala	Ala	Leu	Trp	Gly	Val	Asn	Leu					
245					250					255										
ctg	gtg	ggg	act	gaa	aat	ggc	ctg	atg	ctt	ttg	gac	cga	agt	ggg	caa	817				
Leu	Val	Gly	Thr	Glu	Asn	Gly	Leu	Met	Leu	Leu	Asp	Arg	Ser	Gly	Gln					
260					265					270										
ggc	aaa	gtc	tat	aat	ctg	atc	aac	cgg	agg	cga	ttt	cag	cag	atg	gat	865				
Gly	Lys	Val	Tyr	Asn	Leu	Ile	Asn	Arg	Arg	Arg	Phe	Gln	Gln	Met	Asp					
275					280					285										
gtg	cta	gag	gga	ctg	aat	gtc	ctt	gtg	aca	att	tca	gga	aag	aag	aat	913				
Val	Leu	Glu	Gly	Leu	Asn	Val	Leu	Val	Thr	Ile	Ser	Gly	Lys	Lys	Asn					
290					295					300										
aag	cta	cga	gtt	tac	tat	ctt	tca	tgg	tta	aga	aac	aga	ata	cta	cat	961				
Lys	Leu	Arg	Val	Tyr	Tyr	Leu	Ser	Trp	Leu	Arg	Asn	Arg	Ile	Leu	His					
305	310					315					320									

106

aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac 1009
 Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp
 325 330 335

ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa 1057
 Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys
 340 345 350

ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct 1105
 Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala
 355 360 365

cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc 1153
 Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu
 370 375 380

cag cac aag cct ctg cta gtt gat ctc acg gta gaa gaa ggt caa aga 1201
 Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg
 385 390 395 400

tta aag gtt att ttt ggt tca cac act ggt ttc cat gta att gat gtt 1249
 Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val
 405 410 415

gat tca gga aac tct tat gat atc tac ata cca tct cat att cag ggc 1297
 Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly
 420 425 430

aat atc act cct cat gct att gtc atc ttg cct aaa 1333
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 435 440

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<211> 444

<212> PRT

<213> Homo sapiens

<400> 14

Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn
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 20 25 30

Glu Ser Ser Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp
 35 40 45

Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala
 50 55 60

Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly
 65 70 75 80

Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu
 85 90 95

107

Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly
 100 105 110
 His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu
 115 120 125
 Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly
 130 135 140
 Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly
 145 150 155 160
 Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg
 165 170 175
 Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser
 180 185 190
 Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala
 195 200 205
 Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr
 210 215 220
 Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys
 225 230 235 240
 Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu
 245 250 255
 Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln
 260 265 270
 Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp
 275 280 285
 Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn
 290 295 300
 Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His
 305 310 315 320
 Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp
 325 330 335
 Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys
 340 345 350
 Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala
 355 360 365
 Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu
 370 375 380
 Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg
 385 390 395 400

108

Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val
 405 410 415

Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly
 420 425 430

Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys
 435 440

<210> 15

<211> 1332

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1332)

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cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca 96
 Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser
 20 25 30

gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat 144
 Glu Ser Ser Glu Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp
 35 40 45

ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct 192
 Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala
 50 55 60

cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg 240
 Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly
 65 70 75 80

ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa 288
 Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu
 85 90 95

gga acc ttg atg att aga gag acg tct gga gag aag aag cga tct ggc 336
 Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly
 100 105 110

cac agt gac agc aat ggc ttt gct ggc cac atc aac ctc cct gac ctg 384
 His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu
 115 120 125

gtg cag cag agc cat tct cca gct gga acc ccg act gag gga ctg ggg 432
 Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly
 130 135 140

109

cgc gtc tca acc cat tcc cag gag atg gac tct ggg act gaa tat ggc	480
Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly	
145 150 155 160	
atg ggg agc agc acc aaa gcc tcc ttc acc ccc ttt gtg gac ccc aga	528
Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg	
165 170 175	
gta tac cag acg tct ccc act gat gaa gat gaa gag gat gag gaa tca	576
Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Glu Ser	
180 185 190	
tca gcc gca gct ctg ttt act agc gaa ctt ctt agg caa gaa cag gcc	624
Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala	
195 200 205	
aaa ctc aat gaa gca aga aag att tcg gtg gta aat gta aac cca acc	672
Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr	
210 215 220	
aac att cgg cct cat agc gac aca cca gaa atc aga aaa tac aag aaa	720
Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys	
225 230 235 240	
cga ttc aac tca gaa ata ctt tgt gca gct ctg tgg ggt gta aac ctt	768
Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu	
245 250 255	
ctg gtg ggg act gaa aat ggc ctg atg ctt ttg gac cga agt ggg caa	816
Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln	
260 265 270	
ggc aaa gtc tat aat ctg atc aac cgg agg cga ttt cag cag atg gat	864
Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp	
275 280 285	
gtg cta gag gga ctg aat gtc ctt gtg aca att tca gga aag aag aat	912
Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn	
290 295 300	
aag cta cga gtt tac tat ctt tca tgg tta aga aac aga ata cta cat	960
Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His	
305 310 315 320	
aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac	1008
Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp	
325 330 335	
ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa	1056
Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys	
340 345 350	
ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct	1104
Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala	
355 360 365	
cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc	1152

110

Pro	Lys	Pro	Tyr	His	Lys	Phe	Met	Ala	Phe	Lys	Ser	Phe	Ala	Asp	Leu	
370						375					380					
cag	cac	aag	cct	ctg	cta	gtt	gat	ctc	acg	gta	gaa	gaa	ggt	caa	aga	1200
Gln	His	Lys	Pro	Leu	Leu	Val	Asp	Leu	Thr	Val	Glu	Glu	Gly	Gln	Arg	
385					390				395						400	
tta	aag	gtt	att	ttt	ggt	tca	cac	act	ggt	ttc	cat	gta	att	gat	gtt	1248
Leu	Lys	Val	Ile	Phe	Gly	Ser	His	Thr	Gly	Phe	His	Val	Ile	Asp	Val	
				405					410					415		
gat	tca	gga	aac	tct	tat	gat	atc	tac	ata	cca	tct	cat	att	cag	ggc	1296
Asp	Ser	Gly	Asn	Ser	Tyr	Asp	Ile	Tyr	Ile	Pro	Ser	His	Ile	Gln	Gly	
			420					425						430		
aat	atc	act	cct	cat	gct	att	gtc	atc	ttg	cct	aaa					1332
Asn	Ile	Thr	Pro	His	Ala	Ile	Val	Ile	Leu	Pro	Lys					
			435				440									